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TECH CENTER 1600/2900

APR 11 200?

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RAW SEQUENCE LISTING               DATE: 04/03/2001
PATENT APPLICATION:  US/09/462,629A    TIME: 08:43:24

Input Set : A:\ES.txt
Output Set: N:\CRF3\04032001\I462629A.raw
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  3 <110> APPLICANT: Seulberger, Harald
  4         Lerchl, Jenms
  5         Schmidt, Ralf-Michael
  6         Krupinska, Karin
  7         Falk, Jon
  9 <120> TITLE OF INVENTION: DNA sequence encoding a hydroxyphenylpyruvate dioxygenase, and its
 10         overproduction in plants
W--> 0 <130> FILE REFERENCE:
 12 <140> CURRENT APPLICATION NUMBER: US 09/462,629A
 13 <141> CURRENT FILING DATE: 2000-01-11
 15 <150> PRIOR APPLICATION NUMBER: PCT/EP98/03832
 16 <151> PRIOR FILING DATE: 1998-06-23
 18 <160> NUMBER OF SEQ ID NOS: 2
 20 <170> SOFTWARE: WordPerfect version 6.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1565
 24 <212> TYPE: DNA
 25 <213> ORGANISM: hppd from barley
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: 9 ... 1313
 31 <400> SEQUENCE: 1
 33 cgcacacc atg ccg ccc acc ccc acc acc ccc gcg gct acc ggc gcc gcc50
 34         Met Pro Pro Thr Pro Thr Thr Pro Ala Ala Thr Gly Ala Ala
 35          1           5                   10
 37 gcc gcg gtg acg ccg gag cac gcg cga ccg cac cga atg gtc cgc ttc98
 38 Ala Ala Val Thr Pro Glu His Ala Arg Pro His Arg Met Val Arg Phe
 39  15              20                  25                  30
 41 aac ccg cgc agc gac cgc ttc cac acg ctc tcc ttc cac cac gtc gag146
 42 Asn Pro Arg Ser Asp Arg Phe His Thr Leu Ser Phe His His Val Glu
 43              35                  40                  45
 45 ttc tgg tgc gcg gac gcc gcc tcc gcc gcc ggc cgc ttc gcg ttc gcg194
 46 Phe Trp Cys Ala Asp Ala Ala Ser Ala Ala Gly Arg Phe Ala Phe Ala
 47          50                  55                  60
 49 ctc ggc gcg ccg ctc gcc gcc agg tcc gac ctc tcc acg ggg aac tcc242
 50 Leu Gly Ala Pro Leu Ala Ala Arg Ser Asp Leu Ser Thr Gly Asn Ser
 51          65                  70                  75
 53 gcg cac gcc tcc cag ctg ctc cgc tcg ggc tcc ctc gcc ttc ctc ttc290
 54 Ala His Ala Ser Gln Leu Leu Arg Ser Gly Ser Leu Ala Phe Leu Phe
 55      80                  85                  90
 57 acc gcg ccc tac gcc aac ggc tgc gac gcc gcc acc gcc tcc ctg ccc338
 58 Thr Ala Pro Tyr Ala Asn Gly Cys Asp Ala Ala Thr Ala Ser Leu Pro
 59  95                  100                 105                 110
 61 tcc ttc tcc gcc gac gcc gcg cgc cgg ttc tcc gcc gac cac ggg atc386
 62 Ser Phe Ser Ala Asp Ala Ala Arg Arg Phe Ser Ala Asp His Gly Ile
 63              115                 120                 125
 65 gcg gtg cgc tcc gta gcg ctg cgc gtc gca gac gcc gcc gag gcc ttc434
```

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66 Ala Val Arg Ser Val Ala Leu Arg Val Ala Asp Ala Ala Glu Ala Phe
67           130             135             140
69 cgc gcc agt cgt cga cgg ggc gcg cgc ccg gcc ttc gcc ccc gtg gac482
70 Arg Ala Ser Arg Arg Arg Gly Ala Arg Pro Ala Phe Ala Pro Val Asp
71           145             150             155
73 ctc ggc cgc ggc ttc gcg ttc gcg gag gtc gag ctc tac ggc gac gtc530
74 Leu Gly Arg Gly Phe Ala Phe Ala Glu Val Glu Leu Tyr Gly Asp Val
75      160             165             170
77 gtg ctc cgc ttc gtc agc cac ccg gac ggc acg gac gtg ccc ttc ttg578
78 Val Leu Arg Phe Val Ser His Pro Asp Gly Thr Asp Val Pro Phe Leu
79 175             180             185             190
81 ccg ggg ttc gag ggc gta acc aac ccg gac gcc gtg gac tac ggc ctg626
82 Pro Gly Phe Glu Gly Val Thr Asn Pro Asp Ala Val Asp Tyr Gly Leu
83           195             200             205
85 acg cgg ttc gac cac gtc gtc ggc aac gtc ccg gag ctt gcc ccc gcc674
86 Thr Arg Phe Asp His Val Val Gly Asn Val Pro Glu Leu Ala Pro Ala
87           210             215             220
89 gca gcc tac atc gcc ggg ttc acg ggg ttc cac gag ttc gcc gag ttc722
90 Ala Ala Tyr Ile Ala Gly Phe Thr Gly Phe His Glu Phe Ala Glu Phe
91           225             230             235
93 acg gcg gag gac gtg ggc acg acc gag agc ggg ctc aac tcg gtg gtg770
94 Thr Ala Glu Asp Val Gly Thr Thr Glu Ser Gly Leu Asn Ser Val Val
95      240             245             250
97 ctc gcc aac aac tcg gag ggc gtg ctg ctg ccg ctc aac gag ccg gtg818
98 Leu Ala Asn Asn Ser Glu Gly Val Leu Leu Pro Leu Asn Glu Pro Val
99 255             260             265             270
101 cac ggc acc aag cgc cgg agc cag ata cag acg ttc ctg gaa cac cac866
102 His Gly Thr Lys Arg Arg Ser Gln Ile Gln Thr Phe Leu Glu His His
103             275             280             285
105 ggc ggc ccg ggc gtg cag cac atc gcg gtg gcc agc agt gac gtg ctc914
106 Gly Gly Pro Gly Val Gln His Ile Ala Val Ala Ser Ser Asp Val Leu
107             290             295             300
109 agg acg ctc agg aag atg cgt gcg cgc tcc gcc atg ggc ggc ttc gac962
110 Arg Thr Leu Arg Lys Met Arg Ala Arg Ser Ala Met Gly Gly Phe Asp
111             305             310             315
113 ttc ctg cca ccc ccg ctg ccg aag tac tac gaa ggc gtg cga cgc ctt1010
114 Phe Leu Pro Pro Pro Leu Pro Lys Tyr Tyr Glu Gly Val Arg Arg Leu
115     320             325             330
117 gcc ggg gat gtc ctc tcg gag gcg cag atc aag gaa tgc cag gag ctg1058
118 Ala Gly Asp Val Leu Ser Glu Ala Gln Ile Lys Glu Cys Gln Glu Leu
119 335             340             345             350
121 ggt gtg ctc gtc gat agg gac gac caa ggg gtg ttg ctc caa atc ttc1106
122 Gly Val Leu Val Asp Arg Asp Asp Gln Gly Val Leu Leu Gln Ile Phe
123             355             360             365
125 acc aag cca gta ggg gac agg ccg acc ttg ttc ctg gag atg atc cag1154
126 Thr Lys Pro Val Gly Asp Arg Pro Thr Leu Phe Leu Glu Met Ile Gln
127             370             375             380
129 agg atc ggg tgc atg gag aag gac gag aga ggg gaa gag tac cag aag1202
130 Arg Ile Gly Cys Met Glu Lys Asp Glu Arg Gly Glu Glu Tyr Gln Lys
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131         385             390             395
133 ggt ggc tgc ggc ggg ttc ggc aaa ggc aac ttc tcc gag ctg ttc aag1250
134 Gly Gly Cys Gly Gly Phe Gly Lys Gly Asn Phe Ser Glu Leu Phe Lys
135     400             405             410
137 tcc att gaa gat tac gag aag tcc ctt gaa gcc aag caa tct gct gca1298
138 Ser Ile Glu Asp Tyr Glu Lys Ser Leu Glu Ala Lys Gln Ser Ala Ala
139 415             420             425             430
141 gtt cag gga tca taggatagaa gctggtcctt gtatcatggt ctcatggagc 1350
142 Val Gln Gly Ser
144 aaaagaaaac aatgttgttt gtaatatgcg tcgcacaatt atatcaatgt tataattggt1410
146 gaagctgaag acagatgtat cctatgtatg atgggtgtaa tggatggtag aggggctcac1470
148 acatgaagaa aatgtagcgt tgacattgtt gtacaatctt gcttgcaagt aaaataaaga1530
150 acagattttg agttctgcaa aaaaaaaaaa aaaaa                      1565
153 <210> SEQ ID NO: 2
154 <211> LENGTH: 434
155 <212> TYPE: PRT
156 <213> ORGANISM: hppd from barley
158 <400> SEQUENCE: 2
160 Met Pro Pro Thr Pro Thr Thr Pro Ala Ala Thr Gly Ala Ala Ala Ala
161   1           5               10              15
163 Val Thr Pro Glu His Ala Arg Pro His Arg Met Val Arg Phe Asn Pro
164             20              25              30
166 Arg Ser Asp Arg Phe His Thr Leu Ser Phe His His Val Glu Phe Trp
167         35              40              45
169 Cys Ala Asp Ala Ala Ser Ala Ala Gly Arg Phe Ala Phe Ala Leu Gly
170     50              55              60
172 Ala Pro Leu Ala Ala Arg Ser Asp Leu Ser Thr Gly Asn Ser Ala His
173 65              70              75              80
175 Ala Ser Gln Leu Leu Arg Ser Gly Ser Leu Ala Phe Leu Phe Thr Ala
176             85              90              95
178 Pro Tyr Ala Asn Gly Cys Asp Ala Ala Thr Ala Ser Leu Pro Ser Phe
179             100             105             110
181 Ser Ala Asp Ala Ala Arg Arg Phe Ser Ala Asp His Gly Ile Ala Val
182         115             120             125
184 Arg Ser Val Ala Leu Arg Val Ala Asp Ala Ala Glu Ala Phe Arg Ala
185     130             135             140
187 Ser Arg Arg Arg Gly Ala Arg Pro Ala Phe Ala Pro Val Asp Leu Gly
188 145             150             155             160
190 Arg Gly Phe Ala Phe Ala Glu Val Glu Leu Tyr Gly Asp Val Val Leu
191             165             170             175
193 Arg Phe Val Ser His Pro Asp Gly Thr Asp Val Pro Phe Leu Pro Gly
194         180             185             190
196 Phe Glu Gly Val Thr Asn Pro Asp Ala Val Asp Tyr Gly Leu Thr Arg
197         195             200             205
199 Phe Asp His Val Val Gly Asn Val Pro Glu Leu Ala Pro Ala Ala Ala
200     210             215             220
202 Tyr Ile Ala Gly Phe Thr Gly Phe His Glu Phe Ala Glu Phe Thr Ala
203 225             230             235             240
205 Glu Asp Val Gly Thr Thr Glu Ser Gly Leu Asn Ser Val Val Leu Ala
```

```
206                245                250                255
208 Asn Asn Ser Glu Gly Val Leu Leu Pro Leu Asn Glu Pro Val His Gly
209                260                265                270
211 Thr Lys Arg Arg Ser Gln Ile Gln Thr Phe Leu Glu His His Gly Gly
212            275                280                285
214 Pro Gly Val Gln His Ile Ala Val Ala Ser Ser Asp Val Leu Arg Thr
215        290                295                300
217 Leu Arg Lys Met Arg Ala Arg Ser Ala Met Gly Gly Phe Asp Phe Leu
218 305                310                315                320
220 Pro Pro Pro Leu Pro Lys Tyr Tyr Glu Gly Val Arg Arg Leu Ala Gly
221            325                330                335
223 Asp Val Leu Ser Glu Ala Gln Ile Lys Glu Cys Gln Glu Leu Gly Val
224            340                345                350
226 Leu Val Asp Arg Asp Asp Gln Gly Val Leu Leu Gln Ile Phe Thr Lys
227            355                360                365
229 Pro Val Gly Asp Arg Pro Thr Leu Phe Leu Glu Met Ile Gln Arg Ile
230        370                375                380
232 Gly Cys Met Glu Lys Asp Glu Arg Gly Glu Glu Tyr Gln Lys Gly Gly
233 385                390                395                400
235 Cys Gly Gly Phe Gly Lys Gly Asn Phe Ser Glu Leu Phe Lys Ser Ile
236            405                410                415
238 Glu Asp Tyr Glu Lys Ser Leu Glu Ala Lys Gln Ser Ala Ala Val Gln
239            420                425                430
241 Gly Ser
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/462,629A

DATE: 04/03/2001
TIME: 08:43:25

Input Set : **A:\ES.txt**
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L:0 M:201 W: Mandatory field data missing, FILE REFERENCE